



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/686,647

DATE: 07/25/2002
TIME: 14:30:35

Input Set : N:\Crf3\RULE60\09686647.raw
Output Set: N:\CRF3\07252002\I686647.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: THE ROCKEFELLER UNIVERSITY

7 (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
8 ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES

THEREOF

10 (iii) NUMBER OF SEQUENCES: 38

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Klauber & Jackson
14 (B) STREET: 411 Hackensack Avenue
15 (C) CITY: Hackensack
16 (D) STATE: New Jersey
17 (E) COUNTRY: USA
18 (F) ZIP: 07601

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/686,647
C--> 28 (B) FILING DATE: 10-Oct-2000

38 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/09/183,374
34 (B) FILING DATE:

36 (A) APPLICATION NUMBER: 08/347,563
37 (B) FILING DATE:

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Jackson Esq., David A.
42 (B) REGISTRATION NUMBER: 26,742

43 (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: 201 487-5800
47 (B) TELEFAX: 201 343-1684

48 (C) TELEX: 133521

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 2793 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: double
57 (D) TOPOLOGY: linear

59 (ii) MOLECULE TYPE: DNA (genomic)

60 (A) DESCRIPTION: Murine ob cDNA

ENTERED

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62 (iii) HYPOTHETICAL: NO
64 (iv) ANTI-SENSE: NO
66 (vi) ORIGINAL SOURCE:
67 (A) ORGANISM: Murine
68 (ix) FEATURE:
69 (A) NAME/KEY: CDS
70 (B) LOCATION: 57..560
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75 GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA 56
77 ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG 104
78 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
79 1 5 10 15
81 TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA 152
82 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
83 20 25 30
85 ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG 200
86 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
87 35 40 45
89 CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT 248
90 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
91 50 55 60
93 GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA 296
94 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
95 65 70 75 80
97 GTC TAT CAA CAG GTC CTC ACC AGC CTG CCT TCC CAA AAT GTG CTG CAG 344
98 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
99 85 90 95
101 ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC 392
102 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
103 100 105 110
105 TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA 440
106 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
107 115 120 125
109 GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG 488
110 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
111 130 135 140
113 GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG 536
114 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
115 145 150 155 160
117 TTG GAT GTT AGC CCT GAA TGC TGA AGTTCAAAG GCCACCAGGC TCCCAAGA 588
118 Leu Asp Val Ser Pro Glu Cys
119 165
121 ATCATGTAGA GGGAAAGAAC CTTGGCTTCC AGGGGTCTTC AGGAGAAGAG AGCCATGTGC 648
123 ACACATCCAT CATTCAATTTC TCTCCCTCCT GTAGACCACC CATCCAAAGG CATGACTCCA 708
125 CAATGCTTGA CTCAAGTTAT CCACACAACT TCATGAGCAC AAGGAGGGC CAGCCTGCAG 768
127 AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG 828
129 TCCCACCTGC TCCGGGTACA TGTTCTCCG TGGGTACACG CTTCGCTGCG GCCCAGGAGA 888
131 GGTGAGGTAG GGATGGTAG AGCCTTGAG CTGTCAGA GTCTTGAGA GCACCGTGAA 948
133 GGCTGCATCC ACACACAGCT GGAAACTCCC AAGCAGCACA CGATGGAAGC ACTTATTAT 1008

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135	TTATTCTGCA	TTCTATTTG	GATGGATCTG	AAGCAAGGCA	TCAGCTTTT	CAGGCTTTGG	1068
137	GGGTCAAGCCA	GGATGAGGAA	GGCTCCTGGG	GTGCTGCTT	CAATCCTATT	GATGGGTCTG	1128
139	CCCGAGGCAA	ACCTAATTTT	TGAGTGAUTG	GAAGGAAGGT	TGGGATCTC	CAAACAAGAG	1188
141	TCTATGCAGG	TAGCGCTCAA	GATTGACCTC	TGGTACTGG	TTTTGTTCT	ATTGTGACTG	1248
143	ACTCTATCCA	AACACGTTG	CAGCGGCATT	GCCGGGAGCA	TAGGCTAGGT	TATTATCAA	1308
145	AGCAGATGAA	TTTTGTCAG	TGTAATATGT	ATCTATGTGC	ACCTGAGGGT	AGAGGATGTG	1368
147	TTAGAGGGAG	GGTGAAGGAT	CCCGAAGTGT	TCTCTGAATT	ACATATGTGT	GGTAGGCTTT	1428
149	TCTGAAAGGG	TGAGGCATT	TCTTACCTCT	GTGGCCACAT	AGTGTGGCTT	TGTGAAAAGG	1488
151	ACAAAGGAGT	TGACTCTTC	CGGAACATT	GGAGTGTACC	AGGCACCCCT	GGAGGGGCTA	1548
153	AAGCTACAGG	CCTTTGTTG	GCATATTGCT	GAGCTCAGGG	AGTGAGGGCC	CCACATTGTA	1608
155	GACAGTGAGC	CCCAAGAAAA	GGGTCCCTGG	TGTAGATCTC	CAAGGTTGTC	CAGGGTTGAT	1668
157	CTCACAATGCC	GTTTCTTAAG	CAGGTAGACG	TTTGCATGCC	AATATGTGGT	TCTCATCTGA	1728
159	TTGGTTCATC	CAAAGTAGAA	CCCTGTCTCC	CACCCATTCT	GTGGGGAGTT	TTGTTCCAGT	1788
161	GGGAATGAGA	AATCACTTAG	CAGATGGTCC	TGAGCCCTGG	GCCAGCACTG	CTGAGGAAGT	1848
163	GCCAGGGCCC	CAGGCCAGGC	TGCCAGAATT	GCCCTTCGGG	CTGGAGGATG	AACAAAGGGG	1908
165	CTTGGGTTTT	TCCATCACCC	CTGCACCCCTA	TGTCACCATC	AAACTGGGGG	GCAGATCAGT	1968
167	GAGAGGACAC	TTGATGGAAA	GCAATACACT	TTAAGACTGA	GCACAGTTTC	GTGCTCAGCT	2028
169	CTGTCTGGTG	CTGTGAGCTA	GAGAAGCTA	CCACATACAT	ATAAAATCA	GAGGCTCATG	2088
171	TCCCTGTGGT	TAGACCTAC	TCGCGGCGBT	GTACTCCACC	ACAGCAGCAC	CGCACCGCTG	2148
173	GAAGTACAGT	GCTGCTTCA	ACAGGTGTGA	AAGAACCTGA	GCTGAGGGTG	ACAGTGCCCA	2208
175	GGGGAACCCCT	GCTTGAGTC	TATTGCATT	ACATACCGCA	TTTCAGGGCA	CATTAGCATC	2268
177	CACTCCTATG	GTAGCACACT	GTTGACAATA	GGACAAGGGG	TAGGGGTTGA	CTATCCCTTA	2328
179	TCCAAAATGC	TTGGGACTAG	AAGAGTTTG	GATTTAGAG	TCTTTTCAGG	CATAGGTATA	2388
181	TTTGAGTATA	TATAAAATGA	GATATCTTG	GGATGGGGCC	CAAGTATAAA	CATGAAGTTC	2448
183	ATTATATATT	CATAATACCG	TATAGACACT	GCTGAAGTG	TAGTTTTATA	CAGTGTTTTA	2508
185	AATAACGTTG	TATGCATGAA	AGACGTTTT	ACAGCATGAA	CCTGTCTACT	CATGCCAGCA	2568
187	CTCAAAAACC	TTGGGTTTT	GGAGCAGTT	GGATCTGGG	TTTCTGTTA	AGAGATGGTT	2628
189	AGCTTATACC	AAAACCATA	ATGGCAAACA	GGCTGCAGGA	CCAGACTGGA	TCCTCAGCCC	2688
191	TGAAGTGTGC	CCTTCAGCC	AGGTCACTACC	CTGTGGAGGT	GAGCGGGATC	AGGTTTTGTG	2748
193	G TGCTAAGAG	AGGAGTTGGA	GGTAGATTT	GGAGGATCTG	AGGGC		2793

196 (2) INFORMATION FOR SEQ ID NO: 2:

197 (i) SEQUENCE CHARACTERISTICS:

198 (A) LENGTH: 167 amino acids

199 (B) TYPE: amino acid

200 (D) TOPOLOGY: linear

202 (ii) MOLECULE TYPE: protein

203 (A) DESCRIPTION: Murine ob polypeptide

205 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

207 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu

208 1 5 10 15

210 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys

211 20 25 30

213 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr

214 35 40 45

216 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro

217 50 55 60

219 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala

220 65 70 75 80

222 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln

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223	85	90	95	
225	Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala			
226	100	105	110	
228	Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro			
229	115	120	125	
231	Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val			
232	130	135	140	
234	Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln			
235	145	150	155	160
237	Leu Asp Val Ser Pro Glu Cys			
238	165			
241	(2) INFORMATION FOR SEQ ID NO: 3:			
243	(i) SEQUENCE CHARACTERISTICS:			
244	(A) LENGTH: 700 base pairs			
245	(B) TYPE: nucleic acid			
246	(C) STRANDEDNESS: double			
247	(D) TOPOLOGY: linear			
249	(ii) MOLECULE TYPE: cDNA			
250	(A) DESCRIPTION: Human ob cDNA where N represents any nucleotide			
252	(iii) HYPOTHETICAL: NO			
254	(iv) ANTI-SENSE: NO			
256	(vi) ORIGINAL SOURCE:			
257	(A) ORGANISM: Human			
259	(ix) FEATURE:			
260	(A) NAME/KEY: CDS			
261	(B) LOCATION: 46..546			
264	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:			
266	NNNGNNNTTG CAAGGCCAA GAAGCCANN NTCCTGGAA GGAAA ATG CAT TGG			54
267	Met His Trp			
268	1			
270	GGA ACC CTG TGC GGA TTC TTG TGG CTT TGG CCC TAT CTT TTC TAT GTC			102
271	Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val			
272	5 10 15			
274	CAA GCT GTG CCC ATC CAA AAA GTC CAA GAT GAC ACC AAA ACC CTC ATC			150
275	Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile			
276	20 25 30 35			
278	AAG ACA ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG CAG TCA GTC			198
279	Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val			
280	40 45 50			
282	TCC TCC AAA CAG AAA GTC ACC GGT TTG GAC TTC ATT CCT GGG CTC CAC			246
283	Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His			
284	55 60 65			
286	CCC ATC CTG ACC TTA TCC AAG ATG GAC CAG ACA CTG GCA GTC TAC CAA			294
287	Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln			
288	70 75 80			
290	CAG ATC CTC ACC AGT ATG CCT TCC AGA AAC GTG ATC CAA ATA TCC AAC			342
291	Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn			
292	85 90 95			
294	GAC CTG GAG AAC CTC CGG GAT CTT CTT CAC GTG CTG GCC TTC TCT AAG			390

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295	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Val	Leu	Ala	Phe	Ser	Lys	
296	100				105				110				115				
298	AGC	TGC	CAC	TTG	CCC	TGG	GCC	AGT	GGC	CTG	GAG	ACC	TTG	GAC	AGC	CTG	438
299	Ser	Cys	His	Leu	Pro	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu	Asp	Ser	Leu	
300					120				125				130				
302	GGG	GGT	GTC	CTG	GAA	GCT	TCA	GGC	TAC	TCC	ACA	GAG	GTG	GTG	GCC	CTG	486
303	Gly	Gly	Val	Leu	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val	Val	Ala	Leu	
304					135				140				145				
306	AGC	AGG	CTG	CAG	GGG	TCT	CTG	CAG	GAC	ATG	CTG	TGG	CAG	CTG	GAC	CTC	534
307	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln	Leu	Asp	Leu	
308					150				155				160				
310	AGC	CCT	GGG	TGC	TGAGGCCTT	GAAGGTCACT	CTTCCTGCAA	GGACTNACGT									585
311	Ser	Pro	Gly	Cys													
312					165												
314	TAAGGGAAGG	AACTCTGGTT	TCCAGGTATC	TCCAGGATTG	AAGAGCATTG	CATGGACACC											645
316	CCTTATCCAG	GACTCTGTCA	ATTTCCTGTA	CTCCTCTAAG	CCACTCTTCC	AAAGG											700

319 (2) INFORMATION FOR SEQ ID NO: 4:

321 (i) SEQUENCE CHARACTERISTICS:

322 (A) LENGTH: 167 amino acids

323 (B) TYPE: amino acid

324 (D) TOPOLOGY: linear

326 (ii) MOLECULE TYPE: protein

327 (A) DESCRIPTION: Human ob polypeptide

329 (vi) ORIGINAL SOURCE:

331 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

333	Met	His	Trp	Gly	Thr	Leu	Cys	Gly	Phe	Leu	Trp	Leu	Trp	Pro	Tyr	Leu	
334	1				5				10				15				

336	Phe	Tyr	Val	Gln	Ala	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	
337					20				25				30				

339	Thr	Leu	Ile	Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	
340					35				40				45				

342	Gln	Ser	Val	Ser	Ser	Lys	Gln	Lys	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	
343					50				55				60				

345	Gly	Leu	His	Pro	Ile	Leu	Thr	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala	
346					65				70			75				80	

348	Val	Tyr	Gln	Gln	Ile	Leu	Thr	Ser	Met	Pro	Ser	Arg	Asn	Val	Ile	Gln	
349					85				90				95				

351	Ile	Ser	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Val	Leu	Ala	
352					100				105				110				

355	Phe	Ser	Lys	Ser	Cys	His	Leu	Pro	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu	
356					115				120				125				

359	Asp	Ser	Leu	Gly	Gly	Val	Leu	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val	
360					130				135				140				

362	Val	Ala	Leu	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln	
363					145				150			155				160	

366	Leu	Asp	Leu	Ser	Pro	Gly	Cys										
367					165												

370 (2) INFORMATION FOR SEQ ID NO: 5:

372 (i) SEQUENCE CHARACTERISTICS:

VERIFICATION SUMMARY DATE: 07/25/2002
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Input Set : N:\Crf3\RULE60\09686647.raw
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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:501 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:521 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:563 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:643 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:665 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:687 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:709 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16
L:824 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:1112 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:1131 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:1152 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:1173 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:1195 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:1215 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:1236 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:1257 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
L:1278 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=37